

OIKE

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/10/006,883

TIME: 10:47:08

Input Set : A:\RTS-0337 Sequence Listing.txt

Output Set: N:\CRF3\12172001\J006883.raw

*see
PP. 5, 6, too**OK ->**Does Not Comply
Corrected Diskette Needed*

20

20

*delete duplicate <220> (Please correct
this in
subsequent
sequence)*

60

120

180

240

300

360

420

469

517

565

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```

76 gac tac ttc tcg gcc gaa gat gcg gag att gtg tgt gcc tgc ccc acc      613
77 Asp Tyr Phe Ser Ala Glu Asp Ala Glu Ile Val Cys Ala Cys Pro Thr
78          50          55          60
80 cag cct gac aag gtc cgc aaa att ctg gac ctg gta cag agc aag ggc      661
81 Gln Pro Asp Lys Val Arg Lys Ile Leu Asp Leu Val Gln Ser Lys Gly
82          65          70          75
84 gag gag gtg tcc gag ttc ttc ctc tac ttg ctc cag caa ctc gca gat      709
85 Glu Glu Val Ser Glu Phe Phe Leu Tyr Leu Leu Gln Gln Leu Ala Asp
86 80          85          90          95
88 gcc tac gtg gac ctc agg cct tgg ctg ctg gag atc ggc ttc tcc cct      757
89 Ala Tyr Val Asp Leu Arg Pro Trp Leu Leu Glu Ile Gly Phe Ser Pro
90          100          105          110
92 tcc ctg ctc act cag agc aaa gtc gtg gtc aac act gac cca gtg agc      805
93 Ser Leu Leu Thr Gln Ser Lys Val Val Val Asn Thr Asp Pro Val Ser
94          115          120          125
96 agg tat acc cag cag ctg cga cac cat ctg ggc cgt gac tcc aag ttc      853
97 Arg Tyr Thr Gln Gln Leu Arg His His Leu Gly Arg Asp Ser Lys Phe
98          130          135          140
100 gtg ctg tgc tat gcc cag aag gag gag ctg ctg ctg gag gag atc tac      901
101 Val Leu Cys Tyr Ala Gln Lys Glu Glu Leu Leu Glu Glu Ile Tyr
102          145          150          155
104 atg gac acc atc atg gag ctg gtt ggc ttc agc aat gag agc ctg ggc      949
105 Met Asp Thr Ile Met Glu Leu Val Gly Phe Ser Asn Glu Ser Leu Gly
106 160          165          170          175
108 agc ctg aac agc ctg gcc tgc ctc ctg gac cac acc acc ggc atc ctc      997
109 Ser Leu Asn Ser Leu Ala Cys Leu Leu Asp His Thr Thr Gly Ile Leu
110          180          185          190
112 aat gag cag ggt gag acc atc ttc atc ctg ggt gat gct ggg gtg ggc      1045
113 Asn Glu Gln Gly Glu Thr Ile Phe Ile Leu Gly Asp Ala Gly Val Gly
114          195          200          205
116 aag tcc atg ctg cta cag cgg ctg cag agc ctc tgg gcc acg ggc cgg      1093
117 Lys Ser Met Leu Leu Gln Arg Leu Gln Ser Leu Trp Ala Thr Gly Arg
118          210          215          220
120 cta gac gca ggg gtc aaa ttc ttc ttc cac ttt cgc tgc cgc atg ttc      1141
121 Leu Asp Ala Gly Val Lys Phe Phe His Phe Arg Cys Arg Met Phe
122          225          230          235
124 agc tgc ttc aag gaa agt gac agg ctg tgt ctg cag gac ctg ctc ttc      1189
125 Ser Cys Phe Lys Glu Ser Asp Arg Leu Cys Leu Gln Asp Leu Leu Phe
126 240          245          250          255
128 aag cac tac tgc tac cca gag cgg gac ccc gag gag gtg ttt gcc ttc      1237
129 Lys His Tyr Cys Tyr Pro Glu Arg Asp Pro Glu Glu Val Phe Ala Phe
130          260          265          270
132 ctg ctg cgc ttc ccc cac gtg gcc ctc ttc acc ttc gat ggc ctg gac      1285
133 Leu Leu Arg Phe Pro His Val Ala Leu Phe Thr Phe Asp Gly Leu Asp
134          275          280          285
136 gag ctg cac tcg gac ttg gac ctg agc cgc gtg cct gac agc tcc tgc      1333
137 Glu Leu His Ser Asp Leu Asp Leu Ser Arg Val Pro Asp Ser Ser Cys
138          290          295          300
140 ccc tgg gag cct gcc cac ccc ctg gtc ttg ctg gcc aac ctg ctc agt      1381

```

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141	Pro	Trp	Glu	Pro	Ala	His	Pro	Leu	Val	Leu	Leu	Ala	Asn	Leu	Leu	Ser	
142		305					310					315					
144	ggg	aag	ctg	ctc	aag	ggg	gct	agc	aag	ctg	ctc	aca	gcc	cgc	aca	ggc	1429
145	Gly	Lys	Leu	Leu	Lys	Gly	Ala	Ser	Lys	Leu	Leu	Thr	Ala	Arg	Thr	Gly	
146	320					325					330					335	
148	atc	gag	gtc	ccg	cgc	cag	ttc	ctg	cgg	aag	aag	gtg	ctt	ctc	cgg	ggc	1477
149	Ile	Glu	Val	Pro	Arg	Gln	Phe	Leu	Arg	Lys	Lys	Val	Leu	Leu	Arg	Gly	
150					340					345					350		
152	ttc	tcc	ccc	agc	cac	ctg	cgc	gcc	tat	gcc	agg	agg	atg	ttc	ccc	gag	1525
153	Phe	Ser	Pro	Ser	His	Leu	Arg	Ala	Tyr	Ala	Arg	Arg	Met	Phe	Pro	Glu	
154					355					360				365			
156	cgg	gcc	ctg	cag	gac	cgc	ctg	ctg	agc	cag	ctg	gag	gcc	aac	ccc	aac	1573
157	Arg	Ala	Leu	Gln	Asp	Arg	Leu	Leu	Ser	Gln	Leu	Glu	Ala	Asn	Pro	Asn	
158			370						375				380				
160	ctc	tgc	agc	ctg	tgc	tct	gtg	ccc	ctc	ttc	tgc	tgg	atc	atc	ttc	cgg	1621
161	Leu	Cys	Ser	Leu	Cys	Ser	Val	Pro	Leu	Phe	Cys	Trp	Ile	Ile	Phe	Arg	
162		385					390					395					
164	tgc	ttc	cag	cac	ttc	cgt	gct	gcc	ttt	gaa	ggc	tca	cca	cag	ctg	ccc	1669
165	Cys	Phe	Gln	His	Phe	Arg	Ala	Ala	Phe	Glu	Gly	Ser	Pro	Gln	Leu	Pro	
166	400					405					410					415	
168	gac	tgc	acg	atg	acc	ctg	aca	gat	gtc	ttc	ctc	ctg	gtc	act	gag	gtc	1717
169	Asp	Cys	Thr	Met	Thr	Leu	Thr	Asp	Val	Phe	Leu	Leu	Val	Thr	Glu	Val	
170					420					425					430		
172	cat	ctg	aac	agg	atg	cag	ccc	agc	agc	ctg	gtg	cag	cgg	aac	aca	cgc	1765
173	His	Leu	Asn	Arg	Met	Gln	Pro	Ser	Ser	Leu	Val	Gln	Arg	Asn	Thr	Arg	
174					435					440				445			
176	agc	cca	gtg	gag	acc	ctc	cac	gcc	ggc	cgg	gac	act	ctg	tgc	tcg	ctg	1813
177	Ser	Pro	Val	Glu	Thr	Leu	His	Ala	Gly	Arg	Asp	Thr	Leu	Cys	Ser	Leu	
178			450					455					460				
180	ggg	cag	gtg	gcc	cac	cgg	ggc	atg	gag	aag	agc	ctc	ttt	gtc	ttc	acc	1861
181	Gly	Gln	Val	Ala	His	Arg	Gly	Met	Glu	Lys	Ser	Leu	Phe	Val	Phe	Thr	
182		465					470					475					
184	cag	gag	gag	gtg	cag	gcc	tcc	ggg	ctg	cag	gag	aga	gac	atg	cag	ctg	1909
185	Gln	Glu	Glu	Val	Gln	Ala	Ser	Gly	Leu	Gln	Glu	Arg	Asp	Met	Gln	Leu	
186	480					485					490					495	
188	ggc	ttc	ctg	cgg	gct	ttg	ccg	gag	ctg	ggc	ccc	ggg	ggt	gac	cag	cag	1957
189	Gly	Phe	Leu	Arg	Ala	Leu	Pro	Glu	Leu	Gly	Pro	Gly	Gly	Asp	Gln	Gln	
190					500					505					510		
192	tcc	tat	gag	ttt	ttc	cac	ctc	acc	ctc	cag	gcc	ttc	ttt	aca	gcc	ttc	2005
193	Ser	Tyr	Glu	Phe	Phe	His	Leu	Thr	Leu	Gln	Ala	Phe	Phe	Thr	Ala	Phe	
194				515						520				525			
196	ttc	ctc	gtg	ctg	gac	gac	agg	gtg	ggc	act	cag	gag	ctg	ctc	agg	ttc	2053
197	Phe	Leu	Val	Leu	Asp	Asp	Arg	Val	Gly	Thr	Gln	Glu	Leu	Leu	Arg	Phe	
198			530					535					540				
200	ttc	cag	gag	tgg	atg	ccc	cct	gcg	ggg	gca	gcg	acc	acg	tcc	tgc	tat	2101
201	Phe	Gln	Glu	Trp	Met	Pro	Pro	Ala	Gly	Ala	Ala	Thr	Thr	Ser	Cys	Tyr	
202		545					550					555					
204	cct	ccc	ttc	ctc	ccg	ttc	cag	tgc	ctg	cag	ggc	agt	ggt	ccg	gcg	cgg	2149
205	Pro	Pro	Phe	Leu	Pro	Phe	Gln	Cys	Leu	Gln	Gly	Ser	Gly	Pro	Ala	Arg	

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206	560					565				570				575					
208	gaa	gac	ctc	ttc	aag	aac	aag	gat	cac	ttc	cag	ttc	acc	aac	ctc	ttc			2197
209	Glu	Asp	Leu	Phe	Lys	Asn	Lys	Asp	His	Phe	Gln	Phe	Thr	Asn	Leu	Phe			
210					580					585				590					
212	ctg	tgc	ggg	ctg	ttg	tcc	aaa	gcc	aaa	cag	aaa	ctc	ctg	cgg	cat	ctg			2245
213	Leu	Cys	Gly	Leu	Leu	Ser	Lys	Ala	Lys	Gln	Lys	Leu	Leu	Arg	His	Leu			
214					595					600				605					
216	gtg	ccc	gcg	gca	gcc	ctg	agg	aga	aag	cgc	aag	gcc	ctg	tgg	gca	cac			2293
217	Val	Pro	Ala	Ala	Ala	Leu	Arg	Arg	Lys	Arg	Lys	Ala	Leu	Trp	Ala	His			
218				610					615					620					
220	ctg	ttt	tcc	agc	ctg	cgg	ggc	tac	ctg	aag	agc	ctg	ccc	cgc	gtt	cag			2341
221	Leu	Phe	Ser	Ser	Leu	Arg	Gly	Tyr	Leu	Lys	Ser	Leu	Pro	Arg	Val	Gln			
222		625					630						635						
224	gtc	gaa	agc	ttc	aac	cag	gtg	cag	gcc	atg	ccc	acg	ttc	atc	tgg	atg			2389
225	Val	Glu	Ser	Phe	Asn	Gln	Val	Gln	Ala	Met	Pro	Thr	Phe	Ile	Trp	Met			
226	640					645					650					655			
228	ctg	cgc	tgc	atc	tac	gag	aca	cag	agc	cag	aag	gtg	ggg	cag	ctg	cgc			2437
229	Leu	Arg	Cys	Ile	Tyr	Glu	Thr	Gln	Ser	Gln	Lys	Val	Gly	Gln	Leu	Ala			
230					660					665					670				
232	gcc	agg	ggc	atc	tgc	gcc	aac	tac	ctc	aag	ctg	acc	tac	tgc	aac	gcc			2485
233	Ala	Arg	Gly	Ile	Cys	Ala	Asn	Tyr	Leu	Lys	Leu	Thr	Tyr	Cys	Asn	Ala			
234				675						680				685					
236	tgc	tcg	gcc	gac	tgc	agc	gcc	ctc	tcc	ttc	gtc	ctg	cat	cac	ttc	ccc			2533
237	Cys	Ser	Ala	Asp	Cys	Ser	Ala	Leu	Ser	Phe	Val	Leu	His	His	Phe	Pro			
238			690					695					700						
240	aag	cgg	ctg	gcc	cta	gac	cta	gac	aac	aac	aat	ctc	aac	gac	tac	ggc			2581
241	Lys	Arg	Leu	Ala	Leu	Asp	Leu	Asp	Asn	Asn	Asn	Leu	Asn	Asp	Tyr	Gly			
242		705					710					715							
244	gtg	cgg	gag	ctg	cag	ccc	tgc	ttc	agc	cgc	ctc	act	gtt	ctc	aga	ctc			2629
245	Val	Arg	Glu	Leu	Gln	Pro	Cys	Phe	Ser	Arg	Leu	Thr	Val	Leu	Arg	Leu			
246	720					725					730					735			
248	agc	gta	aac	cag	atc	act	gac	ggt	ggg	gta	aag	gtg	cta	agc	gaa	gag			2677
249	Ser	Val	Asn	Gln	Ile	Thr	Asp	Gly	Gly	Val	Lys	Val	Leu	Ser	Glu	Glu			
250				740						745					750				
252	ctg	acc	aaa	tac	aaa	att	gtg	acc	tat	ttg	ggt	tta	tac	aac	aac	cag			2725
253	Leu	Thr	Lys	Tyr	Lys	Ile	Val	Thr	Tyr	Leu	Gly	Leu	Tyr	Asn	Asn	Gln			
254				755						760				765					
256	atc	acc	gat	gtc	gga	gcc	agg	tac	gtc	acc	aaa	atc	ctg	gat	gaa	tgc			2773
257	Ile	Thr	Asp	Val	Gly	Ala	Arg	Tyr	Val	Thr	Lys	Ile	Leu	Asp	Glu	Cys			
258			770					775					780						
260	aaa	ggc	ctc	acg	cat	ctt	aaa	ctg	gga	aaa	aac	aaa	ata	aca	agt	gaa			2821
261	Lys	Gly	Leu	Thr	His	Leu	Lys	Leu	Gly	Lys	Asn	Lys	Ile	Thr	Ser	Glu			
262		785					790					795							
264	gga	ggg	aag	tat	ctc	gcc	ctg	gct	gtg	aag	aac	agc	aaa	tca	atc	tct			2869
265	Gly	Gly	Lys	Tyr	Leu	Ala	Leu	Ala	Val	Lys	Asn	Ser	Lys	Ser	Ile	Ser			
266	800					805					810					815			
268	gag	gtt	ggg	atg	tgg	ggc	aat	caa	gtt	ggg	gat	gaa	gga	gca	aaa	gcc			2917
269	Glu	Val	Gly	Met	Trp	Gly	Asn	Gln	Val	Gly	Asp	Glu	Gly	Ala	Lys	Ala			
270					820					825						830			

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```

272 ttc gca gag gct ctg cgg aac cac ccc agc ttg acc acc ctg agt ctt 2965
273 Phe Ala Glu Ala Leu Arg Asn His Pro Ser Leu Thr Thr Leu Ser Leu
274      835      840      845
276 gcg tcc aac ggc atc tcc aca gaa gga aag agc ctt gcg agg gcc 3013
277 Ala Ser Asn Gly Ile Ser Thr Glu Gly Gly Lys Ser Leu Ala Arg Ala
278      850      855      860
280 ctg cag cag aac acg tct cta gaa ata ctg tgg ctg acc caa aat gaa 3061
281 Leu Gln Gln Asn Thr Ser Leu Glu Ile Leu Trp Leu Thr Gln Asn Glu
282      865      870      875
284 ctc aac gat gaa gtg gca gag agt ttg gca gaa atg ttg aaa gtc aac 3109
285 Leu Asn Asp Glu Val Ala Glu Ser Leu Ala Glu Met Leu Lys Val Asn
286 880      885      890      895
288 cag acg tta aag cat tta tgg ctt atc cag aat cag atc aca gct aag 3157
289 Gln Thr Leu Lys His Leu Trp Leu Ile Gln Asn Gln Ile Thr Ala Lys
290      900      905      910
292 ggg act gcc cag ctg gca gat gcg tta cag agc aac act ggc ata aca 3205
293 Gly Thr Ala Gln Leu Ala Asp Ala Leu Gln Ser Asn Thr Gly Ile Thr
294      915      920      925
296 gag att tgc cta aat gga aac ctg ata aaa cca gag gag gcc aaa gtc 3253
297 Glu Ile Cys Leu Asn Gly Asn Leu Ile Lys Pro Glu Glu Ala Lys Val
298      930      935      940
300 tat gaa gat gag aag cgg att atc tgt ttc tga gaggatgctt tcctgttcat 3306
301 Tyr Glu Asp Glu Lys Arg Ile Ile Cys Phe
302      945      950
304 ggggtttttg ccttgaggcc tcagcagcaa atgccactct gggcagtcctt ttgtgtcagt 3366
306 gtcttaaagg ggccctgcgca ggcgggacta tcaggagtcct actgcctcca tgatgcaagc 3426
308 cagcttcctg tgcagaaggt ctggtcggca aactccctaa gtaccgcgcta caattctgca 3486
310 gaaaaagaat gtgtcttgcg agctgttgta gttacagtaa atacactgtg aagagacttt 3546
312 attgcctatt ataattattt ttatctgaag ctagaggaat aaagctgtga gcaaacagag 3606
314 gaggccagcc tcacctcatt ccaacacctg ccatagggac caacgggagc gagttggtca 3666
316 ccgctctttt cattgaagag ttgaggatgt ggcacaaagt tgggtgccaag cttcttgaat 3726
318 aaaacgtggt tgatggatta gtattatacc tgaaatattt tcttccttct cagcactttc 3786
320 ccatgtattg atactggtcc cacttcacag ctggagacac cggagtatgt gcagtgtggg 3846
322 atttgactcc tccaagggtt tgtggaaagt taatgtcaag gaaaggatgc accacgggct 3906
324 ttttaatttta atcctggagt ctactgtct gctggcaaat atagagaatg ccctcagctc 3966
326 ttagctggtc taagaatgac gatgccttca aaatgctgct tccactcagg gcttctcctc 4026
328 tgctaggcta cctcctcta gaagcttgag taccatgggc tacagtgtct ggccttgga 4086
330 agaagtgatt ctgtccctcc aaagaaatag ggcattggctt gcccctgtgg ccctggcatc 4146
332 caaatggctg cttttgtctc cttacctcg tgaagagggg aagtctcttc ctgcctccca 4206
334 agcagctgaa ggggtgactaa acgggcgcca agactcaggg gatcggctgg gaactgggcc 4266
336 agcagagcat gttggacacc cccaccatg gtgggcttgt ggtggctgct ccatgagggt 4326
338 gggggtgata ctactagatc acttgtctc ttgcccgtc atttgtaaat aaaatactga 4386
340 aaac 4390
343 <210> SEQ ID NO: 4
344 <211> LENGTH: 19
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
350 <223> OTHER INFORMATION: PCR Primer

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

<210> 13

~~<211> 000~~

~~<212> DNA~~

~~<213> Homo sapiens~~

~~<220>~~

<400> 13

000

delete all this - see item 8

on Ena Summary

Sheet

for proper format

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,883

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:428 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:1166 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:1170 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1375 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:1388 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:1394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1808 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1820 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1824 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1832 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1840 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:3507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95
L:3615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:96

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 16/006 883

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5* amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 1 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
use this format
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
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- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.